

FIG. 1A

Input file Fbh55053e.seq;Output File 55053.trans
Sequence length 2862

GTCGACCCACGCTCCGGACGCGTGGCGGACGCGTGGCGG

ACGCGTCCGGGGACCGGTCTGGGCGGGACCAAGGCACC	ATG	TCC	GGG	GCC	AAG	GAG	GGA	GGT	27											
G	G	S	P	A	Y	H	L	P	H	P	Q	H	A	Q	29					
GGG	GGC	TCT	CCC	GCC	TAC	CAC	CTC	CCC	CAC	CCC	CCA	CCC	CAG	CAC	GCC	CAA	87			
Y	V	G	P	Y	R	L	E	K	T	L	G	K	G	Q	T	G	L	V	K	49
TAT	GTG	GGC	CCC	TAT	CGG	CTG	GAG	AAG	ACG	CTG	GGC	AAA	GGA	CAG	ACA	GGG	CTG	GTT	AAA	147
L	G	V	H	C	I	T	G	Q	K	V	A	I	K	I	V	N	R	E	K	69
CTC	GGG	GTC	CAC	TGC	ATC	ACG	GGT	CAG	AAG	GTC	GCC	ATC	AAG	ATC	GTG	AAC	CGG	GAG	AAG	207
L	S	E	S	V	L	M	K	V	E	R	E	I	A	I	L	K	L	I	E	89
CTG	TCG	GAG	TCG	GTG	CTG	ATG	AAG	GTG	GAG	CGG	GAG	ATC	GCC	ATC	CTG	AAG	CTC	ATC	GAA	267
H	P	H	V	L	K	L	H	D	V	Y	E	N	K	K	Y	L	Y	L	V	109
CAC	CCA	CAT	GTC	CTC	AAG	CTC	CAC	GAC	GTC	TAC	GAG	AAC	AAG	AAA	TAT	TTG	TAC	CTG	GTT	327
L	E	H	V	S	G	G	E	L	F	D	Y	L	V	K	K	G	R	L	T	129
CTG	GAG	CAC	GTC	TCG	GGG	GGT	GAG	CTA	TTC	GAC	TAC	CTG	GTA	AAG	AAG	GGG	AGA	CTG	ACG	387
P	K	E	A	R	K	F	F	R	Q	I	V	S	A	L	D	F	C	H	S	149
CCC	AAG	GAG	GCC	CGA	AAG	TTC	TTC	CGC	CAG	ATT	GTG	TCT	GCG	CTG	GAC	TTC	TGC	CAC	AGC	447



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Docket No.: MPI00-475PIRM

FIG. 1B

Y	S	I	C	H	R	D	L	K	P	E	N	L	L	L	D	E	K	N	N	169
TAC	TCC	ATC	TGC	CAC	AGA	GAC	CTA	AAG	CCC	GAG	AAC	CTG	CTT	TTG	GAT	GAG	AAA	AAC	AAC	507
I	R	I	A	D	F	G	M	A	S	L	Q	V	G	D	S	L	L	E	T	189
ATC	CGC	ATT	GCA	GAC	TTC	GGC	ATG	GCG	TCC	CTG	CAG	GTG	GGG	GAC	AGC	CTC	CTG	GAG	ACC	567
S	C	G	S	P	H	Y	A	C	P	E	V	I	K	G	E	K	Y	D	G	209
AGC	TGC	GGG	TCC	CCC	CAT	TAT	GCG	TGT	CCA	GAG	GTG	ATT	AAG	GGG	GAA	AAA	TAT	GAT	GGC	627
R	R	A	D	M	W	S	C	G	V	I	L	F	A	L	L	V	G	A	L	229
CGC	CGG	GCA	GAC	ATG	TGG	AGC	TGT	GGA	GTC	ATC	CTC	TTC	GCC	CTG	CTC	GTG	GGG	GCT	CTG	687
P	F	D	D	D	N	L	R	Q	L	L	E	K	V	K	R	G	V	F	H	249
CCC	TTT	GAT	GAC	GAC	AAC	CTC	CGC	CAG	CTG	CTG	GAG	AAG	GTG	AAA	CGG	GGC	GTC	TTC	CAC	747
M	P	H	F	I	P	P	D	C	Q	S	L	L	R	G	M	I	E	V	E	269
ATG	CCC	CAC	TTC	ATT	CCT	CCA	GAT	TGC	CAG	AGC	CTC	CTG	AGG	GGA	ATG	ATC	GAA	GTG	GAG	807
P	E	K	R	L	S	L	E	Q	I	Q	K	H	P	W	Y	L	G	G	K	289
CCC	GAA	AAA	AGG	CTC	AGT	CTG	GAG	CAA	ATT	CAG	AAA	CAT	CCT	TGG	TAC	CTA	GGC	GGG	AAA	867
H	E	P	D	P	C	L	E	P	A	P	G	R	R	V	A	M	R	S	L	309
CAC	GAG	CCA	GAC	CCG	TGC	CTG	GAG	CCA	GCC	CCT	GGC	CGC	CGG	GTA	GCC	ATG	CGG	AGC	CTG	927
P	S	N	G	E	L	D	P	D	V	L	E	S	M	A	S	L	G	C	F	329
CCA	TCC	AAC	GGA	GAG	CTG	GAC	CCC	GAC	GTC	CTA	GAG	AGC	ATG	GCA	TCA	CTG	GGC	TGC	TTC	987



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FIG. 1D

R	S	S	G	G	T	P	L	H	S	P	L	H	T	P	R	A	S	P	T	529
CGC	TCC	TCT	GGC	GGG	ACC	CCC	TTG	CAC	TCG	CCT	CTG	CAC	ACG	CCC	CGG	GCC	AGT	CCC	ACC	1587
G	T	P	G	T	T	P	P	P	S	P	G	G	G	V	G	G	A	A	W	549
GGG	ACC	CCG	GGG	ACA	ACA	CCA	CCC	CCC	AGC	CCC	GGC	GGT	GGC	GTC	GGG	GGA	GCC	GCC	TGG	1647
R	S	R	L	N	S	I	R	N	S	F	L	G	S	P	R	F	H	R	R	569
AGG	AGT	CGT	CTC	AAC	TCC	ATC	CGC	AAC	AGC	TTC	CTG	GGC	TCC	CCT	CGC	TTT	CAC	CGG	CGC	1707
K	M	Q	V	P	T	A	E	E	M	S	S	L	T	P	E	S	S	P	E	589
AAG	ATG	CAG	GTC	CCT	ACC	GCT	GAG	GAG	ATG	TCC	AGC	TTG	ACG	CCA	GAG	TCC	TCC	CCG	GAG	1767
L	A	K	R	S	W	F	G	N	F	I	S	L	D	K	E	E	Q	I	F	609
CTG	GCA	AAA	CGC	TCC	TGG	TTC	GGG	AAC	TTC	ATC	TCC	TTG	GAC	AAA	GAA	GAA	CAA	ATA	TTC	1827
L	V	L	K	D	K	P	L	S	S	I	K	A	D	I	V	H	A	F	L	629
CTC	GTG	CTA	AAG	GAC	AAA	CCT	CTC	AGC	AGC	ATC	AAA	GCA	GAC	ATC	GTC	CAT	GCC	TTT	CTG	1887
S	I	P	S	L	S	H	S	V	L	S	Q	T	S	F	R	A	E	Y	K	649
TCG	ATC	CCC	AGC	CTG	AGT	CAC	AGT	GTG	CTG	TCA	CAG	ACC	AGC	TTC	AGG	GCC	GAG	TAC	AAG	1947
A	S	G	G	P	S	V	F	Q	K	P	V	R	F	Q	V	D	I	S	S	669
GCC	AGT	GGC	GGC	CCC	TCC	GTC	TTT	CAA	AAG	CCC	GTC	CGC	TTC	CAG	GTG	GAC	ATC	AGC	TCC	2007
S	E	G	P	E	P	S	P	R	R	D	G	S	G	G	G	G	I	Y	S	689
TCT	GAG	GGT	CCA	GAG	CCC	TCC	CCG	CGA	CGG	GAC	GGC	AGC	GGA	GGT	GGT	GGC	ATC	TAC	TCC	2067



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FIG. 1E

V	T	F	T	L	I	S	G	P	S	R	R	F	K	R	V	V	E	T	I	709
GTC	ACC	TTC	ACT	CTC	ATC	TCG	GGT	CCC	AGC	CGT	CGG	TTC	AAG	CGA	GTG	GTG	GAG	ACC	ATC	2127
Q	A	Q	L	L	S	T	H	D	Q	P	S	V	Q	A	L	A	D	E	K	729
CAG	GCA	CAG	CTC	CTG	AGC	ACT	CAT	GAC	CAG	CCC	TCC	GTG	CAG	GCC	CTG	GCA	GAC	GAG	AAG	2187
N	G	A	Q	T	R	P	A	G	A	P	P	R	S	L	Q	P	P	P	G	749
AAC	GGG	GCC	CAG	ACC	CGG	CCT	GCT	GGT	GCC	CCA	CCC	CGA	AGC	CTG	CAG	CCC	CCA	CCC	GGC	2247
R	P	D	P	E	L	S	S	S	P	R	R	G	P	P	K	D	K	K	L	769
CGC	CCA	GAC	CCA	GAG	CTG	AGC	AGC	TCT	CCC	CGC	CGA	GGC	CCC	CCC	AAG	GAC	AAG	AAG	CTC	2307
L	A	T	N	G	T	P	L	P	*											779
CTG	GCC	ACC	AAC	GGG	ACC	CCT	CTG	CCC	TGA											2337

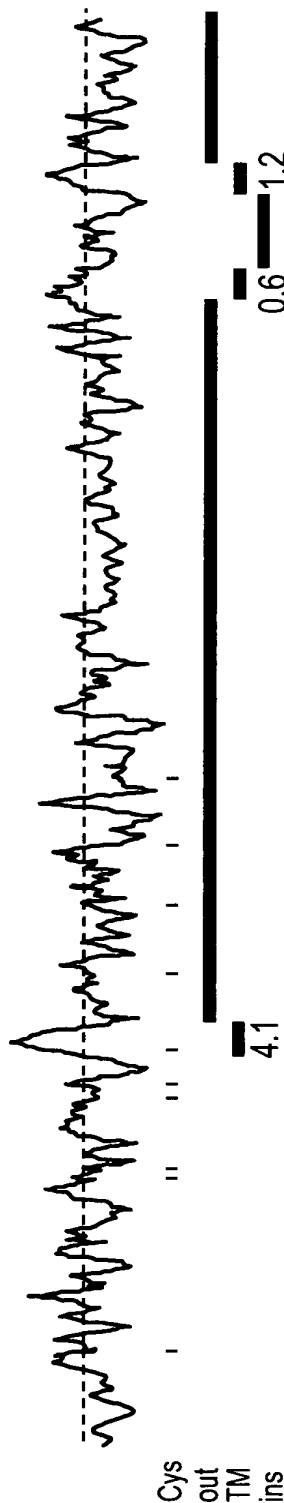
CCCCACGGGCGGGAGGGAGGGACCCCCCTCCACCCCCCTCCGTCGCCCCCAACTGTGAATCTGTAAATAAGGCC
CAAGGAACATGTGCGGAGGGGGTGGACACAAAACCGGCCCTTGCCCTGCAGGGATGGGGCTCCACAGGCCGTGCCCAA
CTGGGGGTGTTCTAGGGGAACAGGGGGCGGGAGCTGTTCTATTATTATTATTATTATTATTATTATTATTATTAT
TGATCAATCTCTCGGGGTGGGGTGGGGAGGACGGAGCTGTTGGGGTGGCTTAGCAGATCCGGACAGGGCCCT
CTGTCCCTGTGTCTCCCAACCCCTCTTCCCGGGCCCTCCCTCCCTGCTCCTCCCAAGACCTTCTGTACGGAT
TTGCTCTCCGGAAGGAATTCTGGTTTCGCGTGATCCTGCCGTCCGTCTCTGTATCCGCGGGCGCAAAAAAAA
AAAAAAA



FIG. 2

Analysis of 55053 (778 aa)

PFAM



>55053

MSSGAKEGGGSPAYHLPHPHPPQHAQYVGPYRLEKTLGKGQGLVKGVLGHVHCITGQKV
AIKIVNREKLSESVLMKVEREIAILKLIHPPHVLKLDVYENKKYLYLVLEHVSGGELFD
YLVKKGRLTPKEARKFFRQIVSALDFCHSYSICHRLKPENLLLDKNNIRIADFGMASL
QVGDSLLETSCGSPHYACPEVIKGEKYDGRADMWSCGVILFALLVGALPFDDNLRQLL
EKVKRGVFHMPHFIPDCQSLRGMIEVEPEKRLSLEQIQKHPWYLGKGHEPDPCLEPAP
GRRVAMRSLPSNGELDPDVLSEMASLGCFRDRERLHRELSEENQEKMIYYLLLDCKER
YPSCEDQDLPPRNDVDPKRVRDSPMLSRHGKRRRPERKSMELVITDAGGGGSPVPTRRRA
LEMAQHSQSRSRVSGASTGLSSSLSSPRSPVFSFSPGAGDEARGGSPSTKTQTLPS
RGPRGGGAGEQPPPSARSTPLPGPPGSPRSSGGTPLHSPHTPRASPTGTPGTTTTPPSP
GGVGGAAWRSRLNSIRNSFLGSPRFHRRKMQVPTAEEMSSLTPESSPELAKRSWFGNFI
SLDKEEQIFLVLDKPLSSIKADIVHAFLSIPSLSHSVLSQTSFRAEYKASGGPSVFQKP
VRFQVDISSSEGPEPSRRDGGGGGIYSVFTLISGSPRRFRVETIQAQLLSTHDQP
SVQALADEKNGAQTRPAGAPRSLQPPPPGRPDPELSSSPRRGPPPKKLLATNGTLP

Transmembrane Segments
Predicted by MEMSAT

Start	End	Orient	Score
214	231	ins->out	4.1
624	640	out->ins	0.6
681	697	ins->out	1.2



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FIG. 3A-1

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM

hmmpfam - search a single seq against HMM database

HMMER 2.1.1 (Dec 1998)

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HMMER is freely distributed under the GNU General Public License (GPL).

HMM file:

/prod/ddm/seqanal/PFAM/pfam5.5/Pfam

Sequence file:

/prod/ddm/wspace/orfanal/oa-script.23506.seq

Query: 55053

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
pkina	Protein kinase domain	323.4	2.6e-93	1
UBA	UBA domain	7.7	4.9	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
pkina	1/1	34	285 ..	1	278 []	323.4	2.6e-93
UBA	1/1	315	356 ..	1	41 []	7.7	4.9



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FIG. 3A-2

Alignments of top-scoring domains:

pkinese: domain 1 of 1, from 34 to 285: score 323.4, E = 2.6e-93

```
*->yelleklGeGsfGkVykakhk.tgkivAvKilkkesls.....lr
y+l ++lG+G G V++++h tg++vA+Ki+++++ls++ + r
55053 34 YRLEKTLGKGQTGLVKLGVHCiTGQKVAIKIVNREKLSesvlmkvER 80

EiGilkrIsHpNIvrlIlgvfedtdhlylvmEymegGdLfdylrrngpls
Ei+ilk + Hp++++l++v+e ++lylv+E++ gG+Lfdyl+++g+l+
55053 81 EIAILKLIIEHPHVLKLHDVYE-NKKYLYLVLEHVSGGELFDYLVKKGRLT 129

ekeakialQilrGleYlHsngivHRDLKpenILLdengtVKiaDFGLAr
+kea++++Qi++++l+++Hs +i+HRDLKpen+llde+++++iaDFG+A
55053 130 PKEARKFFRQIVSALDFCHSYSICHRLDKPENLLLDEKNNIRIADFGMAS 179

ll...eklttfvGTpwYmmAPEvileg.rgysskvDvWSlGvilyElltg
1 +++ 1 t +G+p+Y PEv ++g++++++D+WS+Gvil+ ll g
55053 180 LQvgdSLLLETSCGSPHYA-CPEV-IKGeKYDGRRADMMWSCGVILFALLVG 227

gplfpgadlpafTggdevdqliifvlklPfsdelpktridpleelfrikk
lPfd d+l++l++ +k
55053 228 -----ALPFDD-----DNLRLLEKVK 244

r.rlpIpsncSeelkdLlkkcLnkDPskRpGsatakeilnhpwf<-*
r+ + p+ +++++++Ll++++++ P+kR+ + ++i +hpw
55053 245 RgVFHMPHFIPDCQSLRLGMIEVEPEKRL---SLEQIQKHPWY 285
```




FIG. 3A-3

UBA: domain 1 of 1, from 315 to 356: score 7.7, E = 4.9
->edeekieqLveMGF..dreevvkALratngngverAaewLlsh<-
d + +e++ ++G +dre+ + lr+ n e+ +++Ll +
55053 315 LDPDVLESMASLGCFrDRERLHRELrSEEN-QEKMIYYLLLD 356

//
Searching for complete domains in SMART
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - -
HMM file: /ddm/robison/smart/smart.all.hmms
Sequence file: /prod/ddm/wspace/orfanal/oa-script.23506.seq
- - - - -
Query: 55053



FIG. 3B-1

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
serkin_6		356.8	2.4e-103	1
tyrkin_6		39.2	2.4e-14	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
serkin_6	1/1	34	285 ..	1	231 []	356.8	2.4e-103
tyrkin_6	1/1	34	286 ..	1	280 []	39.2	2.4e-14

Alignments of top-scoring domains:

serkin_6: domain 1 of 1, from 34 to 285: score 356.8, E = 2.4e-103

*->YellkklGkGaFGkVylardkktgrlvAiKvik.....erilr

Y+1 k+lGkG G V+l+++ tg++vAiK++++++ +++ ++r

55053 34 YRLEKTLGKGQTGLVKLVGHVCITGQKVAIKIVNreklsevlMKVER 80

Eikilkk.dHPNIVkLydvfed.dklylVmEyceGdlGdlfdllkkrgr

Ei+iLk HP++ kL+dv+e+++++lylV+E+++G G+Lfd+l+k+gr

55053 81 EIAILKLiEHPHVLKLHDVYENkKYLYLVLEHVSG--GELFDYLVKKGR- 127

glrkvlsE.earfyfrQilsaLeYLHsqgIiHRDLKPeNiLLds..hvKl

l+++ear++frQi+saL+++Hs I+HRDLKPeN+LLd+++++ +

55053 128 -----LTPkEARKFFRQIVSALDFCHSYSICHRLKPeNLLDeKnNIRI 172



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FIG. 3B-2

```
55053 aDFGlaRql.....ttfvGTpeYmAPEvl...gYgkpavDiWSlGcily
      aDFG+A + +++ t +G+p+Y PEv++++++Y+++++D+WS+G+il+
      173 ADFGMASLQvgdsllETSCGSPHYACPEVIkgeKYDGRRADMWSCGVILF 222

      ElltGkpPFp..qldlifkkg.....SpeakdLikklLvkdPek
      ll+G PF+++++l +++++k++++ + ++ +p++ +L++++ +++Pek
      55053 ALLVGALPFDDdNLRQLLEKVKrgvfhmphfiPPDCQSLLRGMIEVEPEK 272

      Rlta.eaLedeldikaHPff<-*
      Rl+ +++ + HP+
      55053 273 RLSleQIQK-----HPWY 285
```



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FIG. 3C

tyrkin_6: domain 1 of 1, from 34 to 286: score 39.2, E = 2.4e-14

*->ltlgkklGeGaFGevykGtlk...ieVAVKtIkeda.....keeFlr

+l+k+LG G+ G V +G+ ++++VA+K ++ ++ +++ ++ r

55053 34 YRLEKTLGKGOTGLVKLGVCitgQKVAIKIVNREKlsesVLMKVER 80

EakiMkklGgkHpNiVklLlGvcteeegrrFmevePlmivmEymegGdLldy

E+ i+k + +Hp++++kL+ v + + l++v+E+++gG L dy

55053 81 EIAILKLI--EHPHVLKLHDVYENK-----KYLVLVLEHVSGGELFDY 121

LrknrpklslsdLlsfAlQIAkMeYLesknfvHRDLAARNcLvgenkvv

L k+++ l++++ +f QI + ++ +s + HRDL N L++e++ +

55053 122 LVKKGR-LTPKEARKFFRQIVSALDFCHSYSICHRLDKPENLLDEKNNI 170

KIsDFGLsRdlyddDkkGeskdYrkkggkggkgtllPirWmAPESlkdgk

+I+DFG++ d + ++ g+ PE++k k

55053 171 RIADFGMASLQVGD-----SLLETSC--GSP-----HYACPEVIKGEK 206

Ft.skSDVWSFGVllWEiftlGeqYPpgeiqqfmsneevleylkkGyRlp

+ + D WS GV L+ ++ G+ P + + +++le++k+G

55053 207 YDgRRADMWSCGVILFALL-VGALPFDD-----DNLRLLEKVKRG-VFH 249

kPendlpisvtCPdelydlmlqCwaedPedRPtFsel...verl<-*

P+ P++ +l + + +Pe+R + ++++++ +l

55053 250 MPHF-----IPPDCCSLLRGMIEVEPEKRLSLEIqkhPWYL 286